

# SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTANOATE

<130>

<140>

<141>

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 325

<212> PRT

<213> Penicillium citrinum

<400> 1

Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro

1 5 10 15

Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr

20 25 30

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp

35 40 45

Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg

50 55 60

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val

65 70 75 80

Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp

85 90 95

Lys Asn Leu Ser Ala  
325

5 <210> 2  
<211> 978  
<212> DNA  
<213> *Penicillium citrinum*

10 <220>  
<221> CDS  
<222> (1).. (978)

<400> 2

15 atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct 48  
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro  
1 5 10 15

20 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96  
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr  
20 25 30

25 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144  
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp  
35 40 45

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192  
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg  
50 55 60

30 gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc 240  
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val  
65 70 75 80

35 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288  
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp  
85 90 95

40 tcc att gac gac tcc ctg aag cgt ctt gga ott gac tac gtt gat atg 336  
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met  
100 105 110

FOOET 15 120001

	Ser	Ile	Asp	Asp	Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Met	
				100					105					110			
5	Phe	Leu	Val	His	Trp	Pro	Ile	Ala	Ala	Glu	Lys	Asn	Gly	Gln	Gly	Glu	
			115					120					125				
	Pro	Lys	Ile	Gly	Pro	Asp	Gly	Lys	Tyr	Val	Ile	Leu	Lys	Asp	Leu	Thr	
		130					135					140					
10	Glu	Asn	Pro	Glu	Pro	Thr	Trp	Arg	Ala	Met	Glu	Lys	Ile	Tyr	Glu	Asp	
	145					150					155					160	
	Arg	Lys	Ala	Arg	Ser	Ile	Gly	Val	Ser	Asn	Trp	Thr	Ile	Ala	Asp	Leu	
5					165					170					175		
	Glu	Lys	Met	Ser	Lys	Phe	Ala	Lys	Val	Met	Pro	His	Ala	Asn	Gln	Ile	
			180						185					190			
	Glu	Ile	His	Pro	Phe	Leu	Pro	Asn	Glu	Glu	Leu	Val	Gln	Tyr	Cys	Phe	
20			195					200					205				
	Ser	Lys	Asn	Ile	Met	Pro	Val	Ala	Tyr	Ser	Pro	Leu	Gly	Ser	Gln	Asn	
		210					215					220					
25	Gln	Val	Pro	Thr	Thr	Gly	Glu	Arg	Val	Ser	Glu	Asn	Lys	Thr	Leu	Asn	
	225					230					235					240	
	Glu	Ile	Ala	Glu	Lys	Gly	Gly	Asn	Thr	Leu	Ala	Gln	Val	Leu	Ile	Ala	
				245						250					255		
30	Trp	Gly	Leu	Arg	Arg	Gly	Tyr	Val	Val	Leu	Pro	Lys	Ser	Ser	Asn	Pro	
				260					265						270		
	Lys	Arg	Ile	Glu	Ser	Asn	Phe	Lys	Ser	Ile	Glu	Leu	Ser	Asp	Ala	Asp	
35			275					280					285				
	Phe	Glu	Ala	Ile	Asn	Ala	Val	Ala	Lys	Gly	Arg	His	Phe	Arg	Phe	Val	
		290					295					300					
40	Asn	Met	Lys	Asp	Thr	Phe	Gly	Tyr	Asp	Val	Trp	Pro	Glu	Glu	Thr	Ala	
	305					310					315					320	

1000415-120601

ttc ctc gti oac tgg ccc att got gcc gag aag aat ggc cag ggt gag 384  
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu  
115 120 125

5 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc 432  
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr  
130 135 140

10 gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat 480  
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp  
145 150 155 160

15 cgc aag gcc agg tcc att ggt gtc tcc aac tgg aac att gcc gac ott 528  
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu  
165 170 175

20 gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc 576  
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile  
180 185 190

gag att oac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc 624  
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe  
195 200 205

25 tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac 672  
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn  
210 215 220

30 cag gtt ccc acc acc ggt gag ogg gtc agc gag aac aag act ctg aac 720  
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn  
225 230 235 240

35 gag atc gcc gag aag ggc ggc aac acc ott got oag gtt ott att goo 768  
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala  
245 250 255

40 tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc 816  
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro  
260 265 270

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864  
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp

1000415-120501

	275	280	285	
	t t t g a a g c c a t c a a t g c c g t t g c c a a g g g t o g t c a c t t c c g t t t c g t c			912
	Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val			
5	290	295	300	
	a a c a t g a a g g a t a c t t t c g g a t a t g a t g t c t g g c c c g a g g a g a c c g c c			960
	Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala			
	305	310	315	320
10	a a g a a c c t g t c t g c g t g a			978
	Lys Asn Leu Ser Ala			
	325			
15	<210> 3			
	<211> 17			
	<212> PRT			
	<213> <i>Penicillium citrinum</i>			
20	<400> 3			
	Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn Gln Val			
	1 5 10 15			
25	Pro			
	<210> 4			
30	<211> 10			
	<212> PRT			
	<213> <i>Penicillium citrinum</i>			
	<400> 4			
35	Ile Pro Gly Val Phe Gly Thr Phe Ala Ser			
	1 5 10			
	<210> 5			
40	<211> 17			
	<212> PRT			
	<213> <i>Penicillium citrinum</i>			

<400> 5

Ser Ile Glu Leu Ser Asp Ala Asp Phe Glu Ala Ile Asn Ala Val Ala  
1 5 10 15

5

Lys

10

<210> 6

<211> 14

<212> PRT

<213> Penicillium citrinum

15

<400> 6

Met Ile Gly Val Ala Asn Tyr Thr Ile Ala Asp Leu Glu Lys  
1 5 10

20

<210> 7

<211> 14

<212> PRT

<213> Penicillium citrinum

25

<400> 7

Tyr Glu Asp Val Leu Xaa Xaa Ile Asp Asp Ser Leu Lys Arg  
1 5 10

30

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

35

<220>

<223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 8

40 ggaacytgrrt tytgswacc

20

5 <210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

10 <400> 9  
 tangonaeng gcataatatt 20

15 <210> 10  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

20 <220>  
 <223> Description of Artificial Sequence:Designed  
 oligonucleotide primer for PCR

25 <400> 10  
 tangnaeng gcataatggt 20

30 <210> 11  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

35 <220>  
 <223> Description of Artificial Sequence:Designed  
 oligonucleotide primer for PCR

40 <400> 11  
 tangnaeng gcatgatatt 20

45 <210> 12  
 <211> 20  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 12

tangcnacng gcattgatgtt

20

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 13

tangcnacng gcatttatatt

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 14

tangcnacng gcatttatgtt

20

<210> 15

<211> 697

<212> DNA

<213> Escherichia coli

<400> 15



```

ogctctaaaa ctantggatc ccccgggctg caggaattog gcggcggogg atccaaogga 60
aanaotttoa cactgagcaa cggcgctcaa attcctggog tcggotttgg taootncgot 120
agtgaagggtt coaagggoga aacotatnct gctgtoccaa ctgocctgaa aacoggttac 180
cgtoncttgg actgtgcctg gtactacctg aacaagggtg aggttgggtga gggnttcogt 240
5 gacttcctga aggaaaacc ctcggtgaag cgtgaggaca tottogtctg caccoagggtg 300
tggaaccacc tccaccgta tgaggacgtc ctctgggtcoa ttgacnacto cctgaagogt 360
cttggaoctg actacgttga tatgttcoto gttcactggc ccattgtctg cgaaaaaat 420
ggccagggtg agcccaaat tggccctgac ggcaaatacn tcnttctcaa ggacctgacc 480
gaaanccna nccacctgg ogogctatgg aaaaaatttn tgangatccc aaggccaggt 540
10 ccattgggtgt ttccaattgg acoattgccg acottgagaa gatgtccaag ttngccaagg 600
tnatgootca cgccaaccag atcgagatto accccttoot gcccacagag gagctgggtgc 660
agtactgctt ttccaagaac antatgcccg tagcgta 697

```

```

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Designed
        oligonucleotide primer for PCR

```

```

<400> 16
ggaggtggtt ccacaccttg g

```

21

```

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Designed
        oligonucleotide primer for PCR

```

```

<400> 17
caaccagato gagattcacc

```

20

```

<210> 18
<211> 331

```

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 18

5 cgctotaaaa ctantggatc ccccgggctg cagggaattcg ggggccgcgg atccttcato 60  
 cccatcatgt otaacggaaa gaotttcaca ttgagcaacg gcgtcaagat tcctggcgctc 120  
 ggctttggta ccttcgctag tgaaggttcc aagggcgaga cctatactgc tgcacooact 180  
 gooctgaaga ccggttaacc tcaattggac tgtgcctggc actacctgaa cgaggggtgag 240  
 gttgggtgagg gtatccgtga cttcctgaag gagaacccct cgggtgaagcg tgaggacato 300  
 10 ttgcgtctgca ccaagggtgtg gaaccacotc c 331

&lt;210&gt; 19

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 19

20 caaccagatc gagattcacc ccttcctgco caacgaggag ctgggtgcagt actgcttctc 60  
 caagaacatt atgocogtgg cctactctcc totgggctcg cagaaccagg ttocaccac 120  
 cgggtgagcgg gtcagcgaga acaagactct gaaogagatc gccgagaagg gcggooaacac 180  
 ccttgctcag gttottattg cctgggggtct gcgcctggc tacgtcgtto tccccaagag 240  
 ctccaacccc aagcgcattg agtccaactt caagagcatt gagctctcog atgccgactt 300  
 tgaagccatc aatgocgttg ccaagggtcg tcaattccgt ttogtcaaca tgaaggatac 360  
 25 tttoggatat gatgtctggc ccgaggagac cgccaagaac ctgtctgctg gaatotctac 420  
 gaaattataa aatnacaccn acnaaaancc aaagcganag gatgatnccc aaaanttttg 480  
 agggtttctt ggttgaaaac gtttantgan cccgaantga angaatagat gancntgatt 540  
 tctccaaaaa aaaaaaaaaa aaaaacggtc cgcggcogct ccnngggggg gcccggttcc 600  
 caattcnccc cttatnattg aattcttttt taanggggnc aaattooncc nnatttcoont 660  
 30 cnanattggn nggcccctc caaactttcn tcnnaaagg gncccaatto ccccccatt 720  
 aantggantt cctntttacc ttt 743

&lt;210&gt; 20

35 &lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

40 <223> Description of Artificial Sequence: Designed  
 orionucleotide primer for PCR

<400> 20  
ccaaggtgtg gaaccacoto c

21

5 <210> 21  
<211> 21  
<212> DNA  
<213> Artificial Sequence

10 <220>  
<223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 21  
15 ccagaggaga gtaggccaog g

21

<210> 22  
<211> 417  
20 <212> DNA  
<213> Escherichia coli

<400> 22  
ccaaggtgtg gaaccacoto caccgttatg aggacgtcot otggtccatt gacgactccc 60  
25 tgaagcgtct tggacttgac tacgttgata tgttccctgt tcaactggccc attgotgocg 120  
agaagaatgg ccagggtgag cccaagattg gccctgaogg caaatacgtc attctcaagg 180  
acctgaccga gaaccccgag cccacatggc gcgctatgga gaagatttat gaggatcgca 240  
aggccaggto cattggtgtc tccaactgga ccattgooga ccttgagaag atgtccaagt 300  
tcgccaaggt catgcctcac gccaacaga tcgagattca ccccttctg cccaacgagg 360  
30 agotggtgca gtactgotto tccaagaaca ttatgccogt ggcctactct cctctgg 417

<210> 23  
<211> 27  
35 <212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 23

gccatggcta tgtotaacgg aaagact

27

<210> 24

5 <211> 29

<212> DNA

<213> Artificial Sequence

<220>

10 <223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 24

oggatccgtt ataatttogt agagattca

29

<210> 25

<211> 21

<212> DNA

20 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 25

gatcatcata gcaggagtca t

21

<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

35 <223> Description of Artificial Sequence: Designed  
oligonucleotide primer for PCR

<400> 26

40 gaattcaaca ccagtcagct c

21

<210> 27  
<211> 786  
<212> DNA  
<213> Escherichia coli

5

<220>  
<221> CDS  
<222> (1).. (786)

10

<400> 27  
atg tat aaa gat tta gaa gga aaa gta gtt gtc ata aca ggt tca tct 48  
Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser  
1 5 10 15

15

acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96  
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala  
20 25 30

20

aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gaa gct aac ago gtt 144  
Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val  
35 40 45

25

tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt 192  
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly  
50 55 60

30

gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att 240  
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile  
65 70 75 80

aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa 288  
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu  
85 90 95

35

aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc 336  
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val  
100 105 110

40

att gat acg aac tta acg gga gca ttt tta ggc ago ogt gaa gcg att 384  
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile  
115 120 125

1000415-130501

aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg 432  
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser  
130 135 140

5 agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca 480  
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala  
145 150 155 160

10 agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac 528  
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr  
165 170 175

15 gct cca aaa ggt att cgt gta aat aac att gga ccg gga gog att aat 576  
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn  
180 185 190

20 aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat 624  
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp  
195 200 205

25 gta gaa ago atg att cca atg gga tac att gga gag ccg gaa gaa att 672  
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile  
210 215 220

30 gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca 720  
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr  
225 230 235 240

35 ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc 768  
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe  
245 250 255

caa gca gga ogc gga taa 786  
Gln Ala Gly Arg Gly  
260

<210> 28

<211> 996

<212> DNA

<213> Penicillium citrinum

<220>

<221> GDS

<222> (1).. (978)

5 <400> 28

atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct 48  
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro  
1 5 10 15

10 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96  
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr  
20 25 30

15 tat act got gtc acc act ggc ctg aag acc ggt tac ogt cac ttg gac 144  
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp  
35 40 45

20 tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192  
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg  
50 55 60

25 gac ttc ctg aag gag aac ccc tog gtg aag ogt gag gac atc ttc gtc 240  
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val  
65 70 75 80

tgc acc aag gtg tgg aac cac ctc ctc cgt tat gag gac gtc ctc tgg 288  
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp  
85 90 95

30 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg 336  
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met  
100 105 110

35 ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag 384  
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu  
115 120 125

40 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc 432  
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr  
130 135 140

gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat 480

1000415-120601

	Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
	145	150 155 160
5	cgc aag gcc agg too att ggt gtc tcc aac tgg acc att gcc gao ctt	528
	Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
	165	170 175
10	gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac oag atc	576
	Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
	180	185 190
15	gag att cac ccc ttc ctg ccc aac gag gag ctg gtg oag tac tgc ttc	624
	Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
	195	200 205
20	tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tgc cag aac	672
	Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
	210	215 220
25	cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
	Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
	225	230 235 240
30	gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768
	Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	
	245	250 255
35	tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816
	Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	
	260	265 270
40	aag cgc att gag too aac ttc aag agc att gag ctc tcc gat gcc gac	864
	Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp	
	275	280 285
45	ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc	912
	Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val	
	290	295 300
50	aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc	960
	Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala	
	305	310 315 320



aag aac ctg tct gcg tga atctctacga aattataa

996

Lys Asn Leu Ser Ala

325

5

<210> 29

<211> 29

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Description of Artificial Sequence Designed oligonucleotide primer for PCR

15

<400> 29

cggtatccgtt caccgagaca ggttcttgg

29

<210> 30

<211> 978

20

<212> DNA

<213> Penicillium citrinum

<220>

<221> GDS

25

<222> (1).. (978)

<400> 30

atg tct aac gga aag act ttc aca ttg ago aac ggc gtc aag att oct 48

Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro

30

1

5

10

15

ggc gtc ggc ttt ggt acc ttc got agt gaa ggt tcc aag ggc gag acc 96

Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr

20

25

30

35

tat act gct gtc acc act gcc ctg aag aac ggt tac ogt cac ttg gao 144

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp

35

40

45

40

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc ogt 192

Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg

50

55

60

10004115-120601

	gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
	Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
	65 70 75 80	
5	tgc acc aag gtg tgg aac ccc ctc cac cgt tat gag gac gtc ctc tgg	288
	Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
	85 90 95	
10	tcc att gac gac tcc ctg aag cgt ott gga ott gac tac gtt gat atg	336
	Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
	100 105 110	
15	ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
	Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
	115 120 125	
20	ccc aag att ggc cct gac gcc aaa tac gtc att ctc aag gac ctg acc	432
	Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
	130 135 140	
25	gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
	Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
	145 150 155 160	
30	cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ott	528
	Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
	165 170 175	
35	gag aag atg tcc aag ttc gcc aag gtc atg oot cac gcc aac cag atc	576
	Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
	180 185 190	
40	gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
	Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
	195 200 205	
45	tcc aag aac att atg ccc gtg gcc tac tot cct ctg gcc tgc cag aac	672
	Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
	210 215 220	
50	cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag aot ctg aac	720

1000415-1000415

	Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
	225 230 235 240	
5	gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	768
	245 250 255	
10	tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	816
	260 265 270	
15	aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp	864
	275 280 285	
20	ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val	912
	290 295 300	
25	aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala	960
	305 310 315 320	
30	aag aac ctg tot gcg tga Lys Asn Leu Ser Ala	978
	325	
35	<210> 31 <211> 27 <212> DNA <213> Artificial Sequence	
40	<220> <223> Description of Artificial Sequence Designed oligonucleotide primer for PCR	
	<400> 31 gccatggcta tgtataaaga tttagaa	27
	<210> 32 <211> 23	

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

5 <223> Description of Artificial Sequence Designed oligonucleotide primer  
for PCR

&lt;400&gt; 32

cggatccggtt atccgogtcc tgc

23

&lt;210&gt; 33

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

15 <223> Description of Artificial Sequence Designed oligonucleotide primer  
for PCR

&lt;400&gt; 33

cggatccgag cgcocaatac gcaaaccg

28

&lt;210&gt; 34

&lt;211&gt; 385

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium sp.

&lt;400&gt; 34

Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr

1

5

10

15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val

20

25

30

35 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro

35

40

45

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly

50

55

60

10004115-120604

	Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile	65	70	75	80
5	Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp		85	90	95
	His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu	100	105	110	
10	Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe	115	120	125	
	Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp	130	135	140	
15	Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His	145	150	155	160
	Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val	165	170	175	
20	Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg	180	185	190	
25	His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys	195	200	205	
	Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp	210	215	220	
30	Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	225	230	235	240
	Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	245	250	255	
35	Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	260	265	270	
40	Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	275	280	285	

FOOTPRINT

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu  
290 295 300

5 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp  
305 310 315 320

Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg  
325 330 335

10

Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr  
340 345 350

15

Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile  
355 360 365

Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro  
370 375 380

20

Arg  
385

25

<210> 35  
<211> 1158  
<212> DNA  
<213> Corynebacterium sp.

30

<220>  
<221> CDS  
<222> (1).. (1158)

<400> 35

35

atg aag gcg atc cag tac acg oga atc ggc gcg gaa ccc gaa ctc acg 48  
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr  
1 5 10 15

40

gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc otg gaa gtc 96  
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val  
20 25 30

acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144

1000445 "STT" 0001

	Thr	Ala	Ala	Gly	Val	Cys	His	Ser	Asp	Asp	Phe	Ile	Met	Ser	Leu	Pro	
				35				40					45				
5	gaa	gag	cag	tac	acc	tac	ggc	ctt	ccg	ctc	acg	ctc	ggc	cac	gaa	ggc	192
	Glu	Glu	Gln	Tyr	Thr	Tyr	Gly	Leu	Pro	Leu	Thr	Leu	Gly	His	Glu	Gly	
			50				55					60					
10	gca	ggc	aag	gtc	gcc	gcc	gtc	ggc	gag	ggg	gtc	gaa	ggg	ctc	gac	atc	240
	Ala	Gly	Lys	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile	
	65					70				75					80		
5	gga	acc	aat	gtc	gtc	gtc	tac	ggg	cct	tgg	ggg	tgc	ggc	aac	tgt	tgg	288
	Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Asn	Cys	Trp	
					85				90					95			
20	cac	tgc	tca	caa	gga	ctc	gag	aac	tat	tgc	tot	cgc	gcc	caa	gaa	ctc	336
	His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Gln	Glu	Leu	
				100				105					110				
25	gga	atc	aat	cct	ccc	ggg	ctc	ggg	gca	ccc	ggc	gcg	ttg	gcc	gag	ttc	384
	Gly	Ile	Asn	Pro	Pro	Gly	Leu	Gly	Ala	Pro	Gly	Ala	Leu	Ala	Glu	Phe	
			115				120					125					
30	atg	atc	gtc	gat	tct	cct	cgc	cac	ctt	gtc	cgc	atc	ggg	gac	ctc	gac	432
	Met	Ile	Val	Asp	Ser	Pro	Arg	His	Leu	Val	Pro	Ile	Gly	Asp	Leu	Asp	
		130					135					140					
35	ccg	gtc	aag	acg	gtg	ccg	ctg	acc	gac	gcc	ggg	ctg	acg	ccg	tat	cac	480
	Pro	Val	Lys	Thr	Val	Pro	Leu	Thr	Asp	Ala	Gly	Leu	Thr	Pro	Tyr	His	
	145					150					155				160		
40	gcg	atc	aag	cgt	tct	ctg	ccg	aaa	ctt	cgc	gga	ggc	tgc	tac	gcg	gtt	528
	Ala	Ile	Lys	Arg	Ser	Leu	Pro	Lys	Leu	Arg	Gly	Gly	Ser	Tyr	Ala	Val	
				165					170					175			
45	gtc	att	ggg	acc	ggc	ggg	ctc	ggc	cac	gtc	got	att	cag	ctc	ctc	cgc	576
	Val	Ile	Gly	Thr	Gly	Gly	Leu	Gly	His	Val	Ala	Ile	Gln	Leu	Leu	Arg	
				180					185					190			
50	cac	ctc	tgc	gcg	gca	acg	gtc	atc	got	ttg	gac	gtg	ago	gog	gac	aag	624
	His	Leu	Ser	Ala	Ala	Thr	Val	Ile	Ala	Leu	Asp	Val	Ser	Ala	Asp	Lys	
			195				200						205				

100011510501

	ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg toc gac	672
	Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp	
	210 215 220	
5	aag gac gcg gcc gag aac gtc ogo aag atc act gga agt caa ggc gcc	720
	Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	
	225 230 235 240	
10	gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg	768
	Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	
	245 250 255	
15	atg gct gtc gcc ggc gtc gga tca gac gtc aag atc gtc ggg atc ggg	816
	Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	
	260 265 270	
20	gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag	864
	Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	
	275 280 285	
25	got tog gtg aca gtt cag tat tgg ggt gcc cgc aac gag ttg atc gaa	912
	Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
	290 295 300	
30	ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc ggc ggt gga gac	960
	Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp	
	305 310 315 320	
35	ott cag tct cga caa cgg tgc cga agc gta tcg acg act ggc tgc cgg	1008
	Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg	
	325 330 335	
40	aac gct cag cgg ccg tgc ggt tgt ggt ccc tgg tct gta gta ccg aca	1056
	Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr	
	340 345 350	
45	gcg gta gaa cga cag cgg aaa aac act gat gcc cgg ccg aat tcg att	1104
	Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile	
	355 360 365	
50	cgg ccg ggc atc agt gtc aga aat tcg gtg tgc got ago tgc acg cct	1152



Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro  
 370 375 380

cga tga

1158

5 Arg  
 385

1000115801